

## **STIC Biotechnology Systems Branch**

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Application Serial Number: 10/583,179  
Source: 1 FWP  
Date Processed by STIC: 6/27/06

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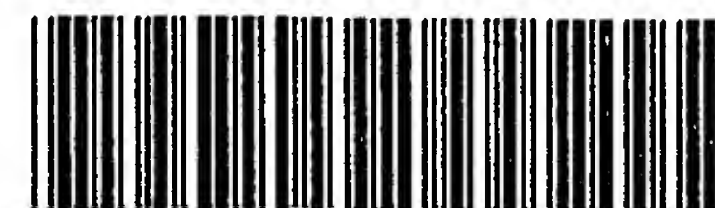
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Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<**<http://www.uspto.gov/efb/efs/downloads/documents.htm>**> , **EFS Submission User Manual - ePAVE**)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
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Revised 01/10/06



IFWP

## RAW SEQUENCE LISTING

DATE: 06/27/2006

PATENT APPLICATION: US/10/583,179

TIME: 12:19:05

Input Set : F:\51571-10 Seq 08-05-06 v1.txt

Output Set: N:\CRF4\06272006\J583179.raw

4 <110> APPLICANT: Agency for Science, Technology and Research  
 6 <120> TITLE OF INVENTION: Protein Separation Device  
 8 <130> FILE REFERENCE: 51571-4  
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/583,179  
 C--> 10 <141> CURRENT FILING DATE: 2006-06-16  
 10 <150> PRIOR APPLICATION NUMBER: US 60/530,608  
 11 <151> PRIOR FILING DATE: 2003-12-19  
 13 <160> NUMBER OF SEQ ID NOS: 8  
 15 <170> SOFTWARE: PatentIn version 3.3  
 18 <210> SEQ ID NO: 1  
 19 <211> LENGTH: 1647  
 20 <212> TYPE: DNA  
 21 <213> ORGANISM: Escherichia coli  
 23 <220> FEATURE:  
 24 <221> NAME/KEY: misc\_feature  
 25 <223> OTHER INFORMATION: GroEL wildtype DNA sequence  
 27 <400> SEQUENCE: 1  
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 29 aacgtactgg cagatgcagt gaaagttacc ctcggtccga aaggccgtaa cgtagttctg 120  
 30 gataaatctt tcggtgcacc gaccatcacc aaagatgggtg tttccgttgc tcgtgaaatc 180  
 31 gaactggaag acaagttcga aaacatgggt gcgcagatgg tgaaagaagt tgcctctaaa 240  
 32 gcgaacgacg ctgcaggcga cggtaccacc actgcaaccg tactggctca ggctatcatc 300  
 33 actgaaggctc tgaaagctgt tgctgcgggc atgaaccgga tggacctgaa acgtggatatc 360  
 34 gacaaagctg ttaccgctgc agttgaagaa ctgaaagcgc tgtccgtacc gtgctctgac 420  
 35 tctaaagcga ttgctcaggt tggctactatc tccgctaact ccgacgaaac cgtaggtaaa 480  
 36 ctgatcgctg aagcgatgga caaagtcggt aaagaaggcg ttatcaccgt tgaagacggt 540  
 37 accggtctgc aggacgaact ggacgtgggt gaaggtatgc agttcgaccg tggctacctg 600  
 38 tctccttact tcatcaacaa gccggaaact ggcgcagtag aactggaaag cccgttcatc 660  
 39 ctgctggctg acaagaaaat ctccaacatc cgcgaaatgc tgccggttct ggaagccggt 720  
 40 gccaaagcag gcaaaccgct gctgatcatc gctgaagatg tagaaggcga agcgtggca 780  
 41 actctgggtg ttaacaccat gcgtggcatc gtgaaagttg ctgcagttaa agctccgggc 840  
 42 ttcggcgatc gtcgtaaagc tatgctgcag gatatcgcaa ccctgactgg cggtagcgta 900  
 43 atctctgaag agatcggtat ggagctggaa aaagcaaccc tgggaagacct gggtcaggct 960  
 44 aaacgcgttg tgatcaacaa agacaccacc accatcatcg atggcgtggg cgaagaagct 1020  
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 47 gtaggtgctg ctaccgaagt tgaaatgaaa gagaaaaaag cacgcgttga agacgcctg 1200  
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 50 aaagttgcac tgcgtgcaat ggaagctccg ctgcgtcaga tcgtcctgaa ctgcggcgaa 1380  
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 53 cgttctgctc tgcagtacgc ggcttctgtg gctggcctga tgatcaccac cgaatgcatg 1560

3-4  
 Does Not Comply  
 Corrected Diskette Needed

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54 gttaccgacc tgccgaaaaa cgatgcagct gacttaggcg ctgctggcgg catgggtggc 1620
55 atgggtggca tgggcggcat gatgtaa 1647
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59 <211> LENGTH: 548
61 <212> TYPE: PRT
62 <213> ORGANISM: Escherichia coli
64 <220> FEATURE:
65 <221> NAME/KEY: misc_feature
66 <223> OTHER INFORMATION: GroEL wildtype amino acid sequence
68 <400> SEQUENCE: 2
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70 1 5 10 15
72 Leu Arg Gly Val Asn Val Leu Ala Asp Ala Val Lys Val Thr Leu Gly
73 20 25 30
75 Pro Lys Gly Arg Asn Val Val Leu Asp Lys Ser Phe Gly Ala Pro Thr
76 35 40 45
78 Ile Thr Lys Asp Gly Val Ser Val Ala Arg Glu Ile Glu Leu Glu Asp
79 50 55 60
81 Lys Phe Glu Asn Met Gly Ala Gln Met Val Lys Glu Val Ala Ser Lys
82 65 70 75 80
84 Ala Asn Asp Ala Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala
85 85 90 95
87 Gln Ala Ile Ile Thr Glu Gly Leu Lys Ala Val Ala Ala Gly Met Asn
88 100 105 110
90 Pro Met Asp Leu Lys Arg Gly Ile Asp Lys Ala Val Thr Ala Ala Val
91 115 120 125
93 Glu Glu Leu Lys Ala Leu Ser Val Pro Cys Ser Asp Ser Lys Ala Ile
94 130 135 140
96 Ala Gln Val Gly Thr Ile Ser Ala Asn Ser Asp Glu Thr Val Gly Lys
97 145 150 155 160
99 Leu Ile Ala Glu Ala Met Asp Lys Val Gly Lys Glu Gly Val Ile Thr
100 165 170 175
102 Val Glu Asp Gly Thr Gly Leu Gln Asp Glu Leu Asp Val Val Glu Gly
103 180 185 190
105 Met Gln Phe Asp Arg Gly Tyr Leu Ser Pro Tyr Phe Ile Asn Lys Pro
106 195 200 205
108 Glu Thr Gly Ala Val Glu Leu Glu Ser Pro Phe Ile Leu Leu Ala Asp
109 210 215 220
111 Lys Lys Ile Ser Asn Ile Arg Glu Met Leu Pro Val Leu Glu Ala Val
112 225 230 235 240
114 Ala Lys Ala Gly Lys Pro Leu Leu Ile Ile Ala Glu Asp Val Glu Gly
115 245 250 255
117 Glu Ala Leu Ala Thr Leu Val Val Asn Thr Met Arg Gly Ile Val Lys
118 260 265 270
121 Val Ala Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys Ala Met
122 275 280 285
124 Leu Gln Asp Ile Ala Thr Leu Thr Gly Gly Thr Val Ile Ser Glu Glu
125 290 295 300
127 Ile Gly Met Glu Leu Glu Lys Ala Thr Leu Glu Asp Leu Gly Gln Ala

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128 305          310          315          320
130 Lys Arg Val Val Ile Asn Lys Asp Thr Thr Thr Ile Ile Asp Gly Val
131          325          330          335
133 Gly Glu Glu Ala Ala Ile Gln Gly Arg Val Ala Gln Ile Arg Gln Gln
134          340          345          350
136 Ile Glu Glu Ala Thr Ser Asp Tyr Asp Arg Glu Lys Leu Gln Glu Arg
137          355          360          365
139 Val Ala Lys Leu Ala Gly Gly Val Ala Val Ile Lys Val Gly Ala Ala
140          370          375          380
142 Thr Glu Val Glu Met Lys Glu Lys Lys Ala Arg Val Glu Asp Ala Leu
143 385          390          395          400
145 His Ala Thr Arg Ala Ala Val Glu Glu Gly Val Val Ala Gly Gly Gly
146          405          410          415
148 Val Ala Leu Ile Arg Val Ala Ser Lys Leu Ala Asp Leu Arg Gly Gln
149          420          425          430
151 Asn Glu Asp Gln Asn Val Gly Ile Lys Val Ala Leu Arg Ala Met Glu
152          435          440          445
154 Ala Pro Leu Arg Gln Ile Val Leu Asn Cys Gly Glu Glu Pro Ser Val
155          450          455          460
157 Val Ala Asn Thr Val Lys Gly Gly Asp Gly Asn Tyr Gly Tyr Asn Ala
158 465          470          475          480
160 Ala Thr Glu Glu Tyr Gly Asn Met Ile Asp Met Gly Ile Leu Asp Pro
161          485          490          495
163 Thr Lys Val Thr Arg Ser Ala Leu Gln Tyr Ala Ala Ser Val Ala Gly
164          500          505          510
166 Leu Met Ile Thr Thr Glu Cys Met Val Thr Asp Leu Pro Lys Asn Asp
167          515          520          525
169 Ala Ala Asp Leu Gly Ala Ala Gly Gly Met Gly Gly Met Gly Gly Met
170          530          535          540
172 Gly Gly Met Met
173 545

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176 &lt;210&gt; SEQ ID NO: 3

177 &lt;211&gt; LENGTH: 1647

178 &lt;212&gt; TYPE: DNA

179 &lt;213&gt; ORGANISM: Escherichia coli

181 &lt;220&gt; FEATURE:

182 &lt;221&gt; NAME/KEY: misc\_feature

183 &lt;223&gt; OTHER INFORMATION: GroEL-Asp490Cys DNA sequence

185 &lt;220&gt; FEATURE:

186 &lt;221&gt; NAME/KEY: mutation

187 &lt;222&gt; LOCATION: (1468)..(1470)

188 &lt;223&gt; OTHER INFORMATION: GAC to TCG

190 &lt;400&gt; SEQUENCE: 3

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191 atggcagcta aagacgtaaa attcggtaac gacgctcgtg tgaaaatgct gcgcggcgta      60
192 aacgtactgg cagatgcagt gaaagttacc ctcggtccga aaggccgtaa cgtagttctg      120
193 gataaatctt tcggtgcacc gaccatcacc aaagatggtg tttccgttgc tcgtgaaatc      180
194 gaactggaag acaagttcga aaacatgggt gcgcagatgg tgaaagaagt tgcctctaaa      240
195 gcgaacgacg ctgcaggcga cggtaccacc actgcaaccg tactggctca ggctatcatc      300
196 actgaaggtc tgaaagctgt tgctgcgggc atgaaccgga tggacctgaa acgtggtatc      360

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*see p. 4 TGC is at locations 1468-1470*

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197 gacaaagctg ttaccgctgc agttgaagaa ctgaaagcgc tgtccgtacc gtgctctgac 420
198 tctaaagcga ttgctcaggt tgggtactatc tccgctaact ccgacgaaac cgtaggtaaa 480
199 ctgatcgctg aagcgatgga caaagtcggt aaagaaggcg ttatcaccgt tgaagacggt 540
200 accggtctgc aggacgaact ggacgtggtt gaaggatgc agttcgaccg tggctacctg 600
201 tctccttact tcatcaacaa gccggaaact ggcgcagtag aactggaaag cccgttcata 660
202 ctgctggctg acaagaaaat ctccaacatc cgcgaaatgc tgccgggttct ggaagccggt 720
203 gccaaagcag gcaaaccgct gctgatcatc gctgaagatg tagaaggcga agcgctggca 780
204 actctgggtg ttaacaccat gcgtggcatc gtgaaagttg ctgcagttaa agctccgggc 840
205 ttcggcgatc gtcgtaaagc tatgctgcag gatatcgcaa ccctgactgg cggtagcgta 900
206 atctctgaag agatcggtat ggagctggaa aaagcaaccc tggagacctt gggtcaggct 960
207 aaacgcgttg tgatcaacaa agacaccacc accatcatcg atggcggtgg cgaagaagct 1020
208 gcaatccagg gccgtgttgc tcagatccgt cagcagattg aagaagcaac ttctgactac 1080
209 gaccgtgaaa aactgcagga gcgcgtagcg aaactggcag gcggcggttc agttatcaaa 1140
210 gtaggtgctg ctaccgaagt tgaaatgaaa gagaaaaaag cacgcgttga agacgccctg 1200
211 cacgcgaccc gtgctgcggt agaagaaggc gtggttgctg gtggtggtgt tgcgctgata 1260
212 cgcgtagcgt ctaaactggc tgacctgcgt ggtcagaacg aagaccagaa cgtgggtata 1320
213 aaagttgcac tgcgtgcaat ggaagctccg ctgcgtcaga tcgtcctgaa ctgcggcgaa 1380
214 gaaccgtctg ttgttgctaa caccgttaaa ggcggcgacg gcaactacgg ttacaacgca 1440
215 gcaaccgaag aatacggcaa catgatcgcg atgggtatcc tggacccaac caaagtaacc 1500
216 cgttctgctc tgcagtacgc ggcttctgtg gctggcctga tgatcaccac cgaatgcatg 1560
217 gttaccgacc tgccgaaaaa cgatgcagct gacttaggcg ctgctggcgg catgggtggc 1620
218 atgggtggca tgggcggcat gatgtaa 1647

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221 &lt;210&gt; SEQ ID NO: 4

222 &lt;211&gt; LENGTH: 548

223 &lt;212&gt; TYPE: PRT

224 &lt;213&gt; ORGANISM: Escherichia coli

226 &lt;220&gt; FEATURE:

227 &lt;221&gt; NAME/KEY: misc\_feature

228 &lt;223&gt; OTHER INFORMATION: GroEL Asp490Cys amino acid sequence

230 &lt;220&gt; FEATURE:

231 &lt;221&gt; NAME/KEY: SITE

232 &lt;222&gt; LOCATION: (490)..(490)

233 &lt;223&gt; OTHER INFORMATION: D to C

235 &lt;400&gt; SEQUENCE: 4

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236 Met Ala Ala Lys Asp Val Lys Phe Gly Asn Asp Ala Arg Val Lys Met
237 1 5 10 15
239 Leu Arg Gly Val Asn Val Leu Ala Asp Ala Val Lys Val Thr Leu Gly
240 20 25 30
241 Pro Lys Gly Arg Asn Val Val Leu Asp Lys Ser Phe Gly Ala Pro Thr
242 35 40 45
244 Ile Thr Lys Asp Gly Val Ser Val Ala Arg Glu Ile Glu Leu Glu Asp
245 50 55 60
247 Lys Phe Glu Asn Met Gly Ala Gln Met Val Lys Glu Val Ala Ser Lys
248 65 70 75 80
250 Ala Asn Asp Ala Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala
251 85 90 95
253 Gln Ala Ile Ile Thr Glu Gly Leu Lys Ala Val Ala Ala Gly Met Asn
254 100 105 110
256 Pro Met Asp Leu Lys Arg Gly Ile Asp Lys Ala Val Thr Ala Ala Val

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Input Set : F:\51571-10 Seq 08-05-06 v1.txt

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257		115		120		125										
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260		130					135					140				
262	Ala	Gln	Val	Gly	Thr	Ile	Ser	Ala	Asn	Ser	Asp	Glu	Thr	Val	Gly	Lys
263	145					150					155				160	
265	Leu	Ile	Ala	Glu	Ala	Met	Asp	Lys	Val	Gly	Lys	Glu	Gly	Val	Ile	Thr
266					165					170					175	
268	Val	Glu	Asp	Gly	Thr	Gly	Leu	Gln	Asp	Glu	Leu	Asp	Val	Val	Glu	Gly
269				180					185					190		
271	Met	Gln	Phe	Asp	Arg	Gly	Tyr	Leu	Ser	Pro	Tyr	Phe	Ile	Asn	Lys	Pro
272			195					200					205			
274	Glu	Thr	Gly	Ala	Val	Glu	Leu	Glu	Ser	Pro	Phe	Ile	Leu	Leu	Ala	Asp
275		210						215				220				
277	Lys	Lys	Ile	Ser	Asn	Ile	Arg	Glu	Met	Leu	Pro	Val	Leu	Glu	Ala	Val
278	225				230						235				240	
280	Ala	Lys	Ala	Gly	Lys	Pro	Leu	Leu	Ile	Ile	Ala	Glu	Asp	Val	Glu	Gly
281					245					250					255	
283	Glu	Ala	Leu	Ala	Thr	Leu	Val	Val	Asn	Thr	Met	Arg	Gly	Ile	Val	Lys
284			260						265					270		
286	Val	Ala	Ala	Val	Lys	Ala	Pro	Gly	Phe	Gly	Asp	Arg	Arg	Lys	Ala	Met
287			275					280				285				
289	Leu	Gln	Asp	Ile	Ala	Thr	Leu	Thr	Gly	Gly	Thr	Val	Ile	Ser	Glu	Glu
290		290					295					300				
292	Ile	Gly	Met	Glu	Leu	Glu	Lys	Ala	Thr	Leu	Glu	Asp	Leu	Gly	Gln	Ala
293	305				310						315				320	
295	Lys	Arg	Val	Val	Ile	Asn	Lys	Asp	Thr	Thr	Thr	Ile	Ile	Asp	Gly	Val
296					325					330					335	
298	Gly	Glu	Glu	Ala	Ala	Ile	Gln	Gly	Arg	Val	Ala	Gln	Ile	Arg	Gln	Gln
299			340						345					350		
301	Ile	Glu	Glu	Ala	Thr	Ser	Asp	Tyr	Asp	Arg	Glu	Lys	Leu	Gln	Glu	Arg
302			355					360					365			
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308	385				390						395				400	
310	His	Ala	Thr	Arg	Ala	Ala	Val	Glu	Glu	Gly	Val	Val	Ala	Gly	Gly	Gly
311					405					410					415	
313	Val	Ala	Leu	Ile	Arg	Val	Ala	Ser	Lys	Leu	Ala	Asp	Leu	Arg	Gly	Gln
314			420						425					430		
316	Asn	Glu	Asp	Gln	Asn	Val	Gly	Ile	Lys	Val	Ala	Leu	Arg	Ala	Met	Glu
317			435					440					445			
319	Ala	Pro	Leu	Arg	Gln	Ile	Val	Leu	Asn	Cys	Gly	Glu	Glu	Pro	Ser	Val
320		450					455					460				
322	Val	Ala	Asn	Thr	Val	Lys	Gly	Gly	Asp	Gly	Asn	Tyr	Gly	Tyr	Asn	Ala
323	465				470						475				480	
325	Ala	Thr	Glu	Glu	Tyr	Gly	Asn	Met	Ile	Cys	Met	Gly	Ile	Leu	Asp	Pro
326					485					490				495		
328	Thr	Lys	Val	Thr	Arg	Ser	Ala	Leu	Gln	Tyr	Ala	Ala	Ser	Val	Ala	Gly
329				500					505					510		

VERIFICATION SUMMARY

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PATENT APPLICATION: US/10/583,179

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Input Set : F:\51571-10 Seq 08-05-06 v1.txt

Output Set: N:\CRF4\06272006\J583179.raw

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L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date